

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/516,478
Source: P4710
Date Processed by STIC: 12/9/04

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PCT

RAW SEQUENCE LISTING

DATE: 12/09/2004

PATENT APPLICATION: US/10/516,478

TIME: 14:23:50

Input Set : A:\PTQ-0041.ST25.txt

Output Set: N:\CRF4\12092004\J516478.raw

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3 <110> APPLICANT: Cancer Care Ontario
4      Lee, Jonathan M.
6 <120> TITLE OF INVENTION: EEF1A2 FOR USE IN F THE PROGNOSIS, DIAGNOSIS AND TREATMENT
OF CANCER
8 <130> FILE REFERENCE: PTQ-0041PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/516,478
C--> 10 <141> CURRENT FILING DATE: 2004-11-30
10 <150> PRIOR APPLICATION NUMBER: US 60/387,231
11 <151> PRIOR FILING DATE: 2002-06-07
13 <160> NUMBER OF SEQ ID NOS: 9
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 14
19 <212> TYPE: PRT
20 <213> ORGANISM: Artificial sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Synthetic
25 <400> SEQUENCE: 1
27 Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
28 1          5          10
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32 <211> LENGTH: 20
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Synthetic
39 <400> SEQUENCE: 2
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43 <210> SEQ ID NO: 3
44 <211> LENGTH: 22
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Synthetic
51 <400> SEQUENCE: 3
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55 <210> SEQ ID NO: 4
56 <211> LENGTH: 19
57 <212> TYPE: DNA
58 <213> ORGANISM: Artificial sequence
60 <220> FEATURE:
61 <223> OTHER INFORMATION: Synthetic
63 <400> SEQUENCE: 4
64 ggttgctgtg ggcttgagt

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Input Set : A:\PTQ-0041.ST25.txt

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67 <210> SEQ ID NO: 5
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69 <212> TYPE: DNA
70 <213> ORGANISM: Homo sapien
72 <400> SEQUENCE: 5
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75 gccgccagtc cctctggctg agacctcggc tccggaatca ctgcagcccc cctcgccctg      120
77 agccagagca ccccggttcc cgccagcccc tcacactccc agcaaaatgg gcaaggagaa      180
79 gacccacatc aacatcgtgg tcatcgccca cgtggactcc ggaaaagtcca ccaccacggg      240
81 ccacctcatc tacaaatgcg gaggtattga caaaaggacc attgagaagt tcgagaagga      300
83 ggcggctgag atggggaagg gatccttcaa gtatgcctgg gtgctggaca agctgaaggc      360
85 ggagcgtgag cgcggcatca ccatcgacat ctccctctgg aagttcgaga ccaccaagta      420
87 ctacatcacc atcatcgatg cccccggcca ccgcgacttc atcaagaaca tgatcacggg      480
89 tacatccacc gcggaatgcg cagtgtgat cgtggcggcg ggcgtgggag agttcgaggc      540
91 gggcatctcc aagaatgggc agacgcggga cgtgccctg ctggcctaca cgctgggtgt      600
93 gaagcagctc atcgtgggcg tgaacaaaat ggactccaca gagccggcct acagcgagaa      660
95 gcgctacgac gagatcgatc aggaagtcag cgcctacatc aagaagatcg gctacaaccc      720
97 ggccaccgtg ccctttgtgc ccatctccgg ctggcacggg gacaacatgc tggagccctc      780
99 cccaacatg ccgtggttca agggctggaa ggtggagcgt aaggagggca acgcaagcgg      840
101 cgtgtccctg ctggaggccc tggacaccat cctgcccccc acgcgccccca cggacaagcc      900
103 cctgcgcctg ccgctgcagg acgtgtacaa gattggcggc attggcacgg tgcccgtggg      960
105 ccggttgagg accggcatcc tgcggccggg catggtggtg acctttgcgc cagtgaacat      1020
107 caccactgag gtgaagtcag tggagatgca ccacgaggct ctgagcgaag ctctgcccgg      1080
109 cgacaacgtc ggcttcaatg tgaagaacgt gtcggtgaag gacatccggc ggggcaacgt      1140
111 gtgtggggac agcaagtctg acccgccgca ggaggctgct cagttcacct cccaggtcat      1200
113 catcctgaac caccgggggc agattagcgc cggctactcc ccggtcatcg actgccacac      1260
115 agccacatc gcctgcaagt ttgcggagct gaaggagaag attgaccggc gctctggcaa      1320
117 gaagctggag gacaacccca agtccctgaa gtctggagac gcggccatcg tggagatggg      1380
119 gccgggaaag cccatgtgtg tggagagctt ctcccagtac ccgcctctcg gccgcttcgc      1440
121 cgtgcgcgac atgaggcaga cgggtggcgt aggcgtcatc aagaacgtgg agaagaagag      1500
123 cggcgccgcc ggcaaggtca ccaagtcggc gcagaaggcg cagaaggcgg gcaagtgaag      1560
125 cgcgggcgcc cgcggcgcca ccctccccgg cggcgccgcy ctccgaaccc cggcccggcc      1620
127 cccgccccgc ccccgccccg cgcgcgcgtc cggcgccccg ccccccgcc aggcgcgtgt      1680
129 ctgcacctcc gcttgccaga ggccctcggg cagcgactgg atgctcgcca tcaaggtcca      1740
131 gtggaagtgc ttcaagagga aaggcgcccc cgcgccaggc ttccgcgccc agcgctcgcc      1800
133 acgctcagtg cccgtttttac caataaactg agcgaccca g                                     1841
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137 <211> LENGTH: 463
138 <212> TYPE: PRT
139 <213> ORGANISM: Homo sapien
141 <400> SEQUENCE: 6
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144 1          5          10          15
147 Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Cys Gly
148          20          25          30
151 Gly Ile Asp Lys Arg Thr Ile Glu Lys Phe Glu Lys Glu Ala Ala Glu
152          35          40          45
155 Met Gly Lys Gly Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
156          50          55          60

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159 Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ser Leu Trp Lys Phe
160 65 70 75 80
163 Glu Thr Thr Lys Tyr Tyr Ile Thr Ile Ile Asp Ala Pro Gly His Arg
164 85 90 95
167 Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
168 100 105 110
171 Val Leu Ile Val Ala Ala Gly Val Gly Glu Phe Glu Ala Gly Ile Ser
172 115 120 125
175 Lys Asn Gly Gln Thr Arg Glu His Ala Leu Leu Ala Tyr Thr Leu Gly
176 130 135 140
179 Val Lys Lys Gln Leu Ile Val Gly Val Asn Lys Met Asp Ser Thr Glu Pro
180 145 150 155 160
183 Ala Tyr Ser Glu Lys Arg Tyr Asp Glu Ile Val Lys Glu Val Ser Ala
184 165 170 175
187 Tyr Ile Lys Lys Ile Gly Tyr Asn Pro Ala Thr Val Pro Phe Val Pro
188 180 185 190
191 Ile Ser Gly Trp His Gly Asp Asn Met Leu Glu Pro Ser Pro Asn Met
192 195 200 205
195 Pro Trp Phe Lys Gly Trp Lys Val Glu Arg Lys Glu Gly Asn Ala Ser
196 210 215 220
199 Gly Val Ser Leu Leu Glu Ala Leu Asp Thr Ile Leu Pro Pro Thr Arg
200 225 230 235 240
203 Pro Thr Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile
204 245 250 255
207 Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Ile Leu
208 260 265 270
211 Arg Pro Gly Met Val Val Thr Phe Ala Pro Val Asn Ile Thr Thr Glu
212 275 280 285
215 Val Lys Ser Val Glu Met His Glu Ala Leu Ser Glu Ala Leu Pro
216 290 295 300
219 Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Ile
220 305 310 315 320
223 Arg Arg Gly Asn Val Cys Gly Asp Ser Lys Ser Asp Pro Pro Gln Glu
224 325 330 335
227 Ala Ala Gln Phe Thr Ser Gln Val Ile Ile Leu Asn His Pro Gly Gln
228 340 345 350
231 Ile Ser Ala Gly Tyr Ser Pro Val Ile Asp Cys His Thr Ala His Ile
232 355 360 365
235 Ala Cys Lys Phe Ala Glu Leu Lys Glu Lys Ile Asp Arg Arg Ser Gly
236 370 375 380
239 Lys Lys Leu Glu Asp Asn Pro Lys Ser Leu Lys Ser Gly Asp Ala Ala
240 385 390 395 400
243 Ile Val Glu Met Val Pro Gly Lys Pro Met Cys Val Glu Ser Phe Ser
244 405 410 415
247 Gln Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr
248 420 425 430
251 Val Ala Val Gly Val Ile Lys Asn Val Glu Lys Lys Ser Gly Gly Ala
252 435 440 445
255 Gly Lys Val Thr Lys Ser Ala Gln Lys Ala Gln Lys Ala Gly Lys

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260 <211> LENGTH: 1837
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapien
264 <400> SEQUENCE: 7
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267 aaatgggaaa ggaaaagact catatcaaca ttgtcgtcat tggacacgta gattcgggca      120
269 agtccaccac tactggccat ctgatctata aatgcggtgg catcgacaaa agaaccattg      180
271 aaaaatttga gaaggaggct gctgagatgg gaaagggctc cttcaagtat gcctgggtct      240
273 tggataaact gaaagctgag cgtgaacgtg gtatcaccat tgatatctcc ttgtggaaat      300
275 ttgagaccag caagtactat gtgactatca ttgatgcccc aggacacaga gactttatca      360
277 aaaacatgat tacagggaca tctcaggctg actgtgctgt cctgattgtt gctgctggtg      420
279 ttggtgaatt tgaagctggg atctccaaga atgggcagac ccgagagcat gcccttctgg      480
281 cttacacact ggggtgtgaaa caactaattg tcggtgttaa caaaatggat tccactgagc      540
283 caccctacag ccagaagaga tatgaggaaa ttgttaagga agtcagcact tacattaaga      600
285 aaattggcta caaccccgac acagtagcat ttgtgccaat ttctggttgg aatggtgaca      660
287 acatgctgga gccaaagtgc aacatgcctt ggttcaaggg atggaaagtc acccgtaagg      720
289 atggcaatgc cagtggaacc acgctgcttg aggctctgga ctgcatccta ccaccaactc      780
291 gtccaactga caagcccttg cgcctgcctc tccaggatgt ctacaaaatt ggtggtattg      840
293 gtactgttcc tgttggccga gtggagactg gtgttctcaa acccggtatg gtggtcacct      900
295 ttgctccagt caacgttaca acggaagtaa aatctgtcga aatgcaccat gaagctttga      960
297 gtgaagctct tcctggggac aatgtgggct tcaatgtcaa gaatgtgtct gtcaaggatg     1020
299 ttcgtcgtgg caacgttgct ggtgacagca aaaatgaccc accaatggaa gcagctggct     1080
301 tcaactgctca ggtgattatc ctgaaccatc caggccaaat aagcgcgggc tatgcccctg     1140
303 tattggattg ccacacggct cacattgcat gcaagtttgc tgagctgaag gaaaagattg     1200
305 atcgccgttc tggtaaaaag ctggaagatg gccctaaatt cttgaagtct ggtgatgctg     1260
307 ccattgttga tatggttcct ggcaagccca tgtgtgttga gagcttctca gactatccac     1320
309 ctttgggtcg ctttgcgtgt cgtgatatga gacagacagt tgcggtgggt gtcatcaaag     1380
311 cagtggacaa gaaggctgct ggagctggca aggtcaccaa gtctgccag aaagctcaga     1440
313 aggtctaaatg aatattatcc ctaatacctg ccacccact cttaatcagt ggtggaagaa     1500
315 cggctctcaga actgtttgtt tcaattggcc atttaagttt agtagtataa gactggttaa     1560
317 tgataacaat gcacgtgtaa accttcagaa ggaaaggaga atgttttgtg gaccactttg     1620
319 gttttctttt ttgcgtgtgg cagtttttaag ttattagttt ttaaaatcag tactttttta     1680
321 tggaaacaac ttgacaaaaa atttgtcaca gaattttgag acccattaaa aaagttaaat     1740
323 gagaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     1800
325 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa                                     1837
328 <210> SEQ ID NO: 8
329 <211> LENGTH: 13
330 <212> TYPE: PRT
331 <213> ORGANISM: Artificial sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Synthetic
336 <400> SEQUENCE: 8
338 Ser His Thr Thr Leu Leu Glu Ala Val Asp Cys Ile Leu
339 1      5      10
342 <210> SEQ ID NO: 9
343 <211> LENGTH: 13
344 <212> TYPE: PRT

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345 <213> ORGANISM: Artificial sequence

347 <220> FEATURE:

348 <223> OTHER INFORMATION: Synthetic

350 <400> SEQUENCE: 9

352 Ser Gly Val Ser Leu Leu Glu Ala Leu Asp Thr Ile Leu

353 1

5

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VERIFICATION SUMMARY

DATE: 12/09/2004

PATENT APPLICATION: US/10/516,478

TIME: 14:23:51

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Output Set: N:\CRF4\12092004\J516478.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date